

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 12:46:54 ; Search time 3 Seconds
(without alignments)
4.063 Million cell updates/sec

Title: frags1-16

Perfect score: 1122

Sequence: 1 cgtctcttcttctgagcct.....aggccgcaggaggaagc 1122

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 329 seqs, 5432 residues

Total number of hits satisfying chosen parameters: 658

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 637 summaries

Database : rng1-16.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	30	2.7	30	1 AAV63648	Antisense oligonuc
C 2	30	2.7	30	1 AAV63649	Antisense oligonuc
C 3	30	2.7	30	1 AAV63649	Antisense oligonuc
C 4	30	2.7	30	1 AAV41175	RNA component of h
C 5	30	2.7	30	1 AAV41175	RNA component of h
C 6	30	2.7	30	1 AAV41175	RNA component of h
C 7	30	2.7	30	1 AAV41172	RNA component of h
C 8	30	2.7	30	1 AAV41172	RNA component of h
C 9	30	2.7	30	1 AAZ23630	Human clone 28-1 t
C 10	30	2.7	30	1 AAZ23631	Human clone 28-1 t
C 11	30	2.7	30	1 AAZ23631	Human clone 28-1 t
C 12	30	2.7	30	1 AAS15928	Human telomerase p
C 13	30	2.7	30	1 AAS15928	Human telomerase p
C 14	30	2.7	30	1 AAS09476	Antisense oligonuc
C 15	30	2.7	30	1 AAS09476	Antisense oligonuc
C 16	30	2.7	30	1 AAS09475	Antisense oligonuc
C 17	30	2.7	30	1 ABA91517	Oligonucleotide us
C 18	30	2.7	30	1 ABA91517	Oligonucleotide us
C 19	30	2.7	30	1 ABX10985	Human telomerase a
C 20	30	2.7	30	1 ABX10986	Human telomerase a
C 21	30	2.7	30	1 ABX10986	Human telomerase a
C 22	30	2.7	30	1 ADC35652	Human telomerase R
C 23	30	2.7	30	1 ADC35652	Human telomerase R
C 24	30	2.7	30	1 ADC35651	Human telomerase R
C 25	30	2.7	30	1 ADC35651	Human telomerase R
C 26	30	2.7	30	1 ADG62873	Human telomerase R
C 27	30	2.7	30	1 ADG62874	Human telomerase R
C 28	27	2.4	27	1 AAV41193	RNA component of h
C 29	27	2.4	27	1 ABA93497	Primer for product
C 30	26	2.3	26	1 AAT10304	RNA component of h
C 31	26	2.3	26	1 AAT10304	RNA component of h
C 32	26	2.3	26	1 AAT10299	RNA component of h
C 33	26	2.3	26	1 AAT58811	Human telomerase p

C 34	26	2.3	26	1 AAV17033	Telomerase PCR pri
C 35	26	2.3	26	1 AAV19489	Human htr gene RT-
C 36	26	2.3	26	1 AAX30788	Human telomerase R
C 37	26	2.3	26	1 AAX77402	PCR primer for Hum
C 38	26	2.3	26	1 AAX01542	Human telomerase R
C 39	26	2.3	26	1 AAX88250	Human telomerase R
C 40	26	2.3	26	1 ABK48024	Human telomerase (
C 41	26	2.3	26	1 AD24246	Human telomerase (
C 42	26	2.3	26	1 ADG82593	Human telomerase p
C 43	25	2.2	25	1 AAC93100	Human telomerase p
C 44	24.4	2.2	30	1 AAV41169	RNA component of h
C 45	24	2.1	25	1 AAZ08704	Human telomerase R
C 46	23	2.0	23	1 ADF93794	Human TERC mRNA tr
C 47	23	2.0	23	1 ADF93793	Human TERC mRNA tr
C 48	23	2.0	23	1 ADF93793	Human TERC mRNA tr
C 49	23	2.0	23	1 ADG29525	htr siNA-target RN
C 50	23	2.0	23	1 ADG29524	htr siNA-target RN
C 51	23	2.0	23	1 ADG29524	htr siNA-target RN
C 52	23	2.0	27	1 AAV41193	RNA component of h
C 53	23	2.0	27	1 ABA95497	Human telomerase R
C 54	22	2.0	22	1 AAT58812	Human telomerase p
C 55	22	2.0	23	1 ADF93795	Human TERC mRNA tr
C 56	22	2.0	23	1 ADF93795	Human TERC mRNA tr
C 57	22	2.0	23	1 ADF93802	Human TERC mRNA tr
C 58	22	2.0	23	1 ADF93802	Human TERC mRNA tr
C 59	22	2.0	23	1 ADG29526	htr siNA-target RN
C 60	22	2.0	23	1 ADG29526	htr siNA-target RN
C 61	22	2.0	23	1 ADG29526	htr siNA-target RN
C 62	22	2.0	23	1 ADG29520	htr siNA-target RN
C 63	22	2.0	25	1 AAZ08704	Human telomerase R
C 64	22	2.0	25	1 AAZ07280	Human telomerase R
C 65	22	2.0	26	1 AAT11044	Primer for product
C 66	22	2.0	26	1 AAT10304	RNA component of h
C 67	22	2.0	26	1 AAT10299	RNA component of h
C 68	22	2.0	26	1 AAT58811	Human telomerase p
C 69	22	2.0	26	1 AAV17033	Telomerase PCR pri
C 70	22	2.0	26	1 AAV19489	Human htr gene RT-
C 71	22	2.0	26	1 AAX90788	Human telomerase R
C 72	22	2.0	26	1 AAX77402	Human telomerase R
C 73	22	2.0	26	1 AAX01542	PCR primer for Hum
C 74	22	2.0	26	1 AAX88250	Human telomerase R
C 75	22	2.0	26	1 ABK48024	Human telomerase a
C 76	22	2.0	26	1 AD24246	Human telomerase (
C 77	22	2.0	26	1 ADG82593	Human telomerase p
C 78	21	1.9	21	1 ADF93860	Human TERC siRNA,
C 79	21	1.9	21	1 ADF93860	Human TERC siRNA,
C 80	21	1.9	21	1 ADG30029	htr-targeted siNA,
C 81	21	1.9	21	1 ADG30029	htr-targeted siNA,
C 82	21	1.9	22	1 ACC57544	Telomerase PCR pri
C 83	21	1.9	22	1 ACC57544	Telomerase PCR pri
C 84	21	1.9	22	1 ADF93794	Human TERC mRNA tr
C 85	21	1.9	23	1 ADG29525	htr siNA-target RN
C 86	20	1.8	20	1 AAV71226	Antisense oligonuc
C 87	20	1.8	20	1 AAV71226	Antisense oligonuc
C 88	20	1.8	20	1 AAV41173	RNA component of h
C 89	20	1.8	20	1 AAV41173	RNA component of h
C 90	20	1.8	20	1 AAV41170	RNA component of h
C 91	20	1.8	20	1 AAV41170	RNA component of h
C 92	20	1.8	20	1 AAV41174	RNA component of h
C 93	20	1.8	20	1 AAV41174	RNA component of h
C 94	20	1.8	20	1 AAV41180	RNA component of h
C 95	20	1.8	20	1 AAV41180	RNA component of h
C 96	20	1.8	20	1 AAZ23632	Human clone 28-1 t
C 97	20	1.8	20	1 AAZ23632	Human clone 28-1 t
C 98	20	1.8	20	1 AAZ23636	Human clone 28-1 t
C 99	20	1.8	20	1 AAZ23636	Human clone 28-1 t
C 100	20	1.8	20	1 AAS15934	Human telomerase p
C 101	20	1.8	20	1 AAS09477	Antisense oligonuc
C 102	20	1.8	20	1 AAS09477	Antisense oligonuc
C 103	20	1.8	20	1 AAS09480	Antisense oligonuc
C 104	20	1.8	20	1 AAS09480	Antisense oligonuc
C 105	20	1.8	20	1 ADF93865	Human TERC siRNA,
C 106	20	1.8	21	1 ADF93865	Human TERC siRNA,

C 253	12.4	1.1	16	1	ADJ36925	Gene 216 related a	C 326	11.4	1.0	14	1	ADQ29792	Rat Vrl1 exon la tr
C 254	12.4	1.1	16	1	ADL81503	Gene 216 ASO prime	C 327	11.4	1.0	14	1	ADQ29847	Murine Vrl1 exon la
C 255	12.4	1.1	16	1	ADL81503	Gene 216 ASO prime	C 328	11.4	1.0	14	1	ADQ29847	Murine Vrl1 exon la
C 256	12	1.1	12	1	AAV41171	RNA component of h	C 329	11.4	1.0	15	1	AAQ29054	Unique 3' PCR prim
C 257	12	1.1	12	1	AAV41171	RNA component of h	C 330	11.4	1.0	15	1	AAQ29054	Unique 3' PCR prim
C 258	12	1.1	12	1	ABH86386	Oligonucleotide pr	C 331	11.4	1.0	15	1	AAQ29054	Human CERP HH ribo
C 259	12	1.1	12	1	ABH86386	Oligonucleotide pr	C 332	11.4	1.0	15	1	AAQ29054	Human CERP HH ribo
C 260	12	1.1	12	1	AAH15935	Human telomerase p	C 333	11.4	1.0	15	1	AAQ29054	Human CERP HH ribo
C 261	12	1.1	13	1	ABC09084	Oligonucleotide SE	C 334	11.4	1.0	15	1	AAQ29054	Human CERP HH ribo
C 262	12	1.1	13	1	ABC09084	Oligonucleotide SE	C 335	11.4	1.0	15	1	AAV48867	Erbb-2 gene antis
C 263	12	1.1	13	1	ABH44170	Oligonucleotide SE	C 336	11.4	1.0	15	1	AAV48867	IGF-1 oligonucleot
C 264	12	1.1	13	1	ABH44170	Oligonucleotide SE	C 337	11.4	1.0	15	1	AAV48867	IGF-1 oligonucleot
C 265	12	1.1	13	1	ABH59432	Oligonucleotide SE	C 338	11.4	1.0	15	1	AAV48867	IGF-1 oligonucleot
C 266	12	1.1	13	1	ABH59432	Oligonucleotide SE	C 339	11.4	1.0	15	1	AAV48867	Human focal adhesi
C 267	12	1.1	13	1	ABH59433	Oligonucleotide SE	C 340	11.4	1.0	15	1	AAV48867	Human focal adhesi
C 268	12	1.1	13	1	ABH59433	Oligonucleotide SE	C 341	11.4	1.0	15	1	AAV48867	Even-skipped homeo
C 269	12	1.1	13	1	ABH44171	Oligonucleotide SE	C 342	11.4	1.0	15	1	AAV48867	Even-skipped homeo
C 270	12	1.1	13	1	ABH44171	Oligonucleotide SE	C 343	11.4	1.0	15	1	AAV48867	Human CYP27A1 gene
C 271	12	1.1	13	1	ABH44171	Oligonucleotide SE	C 344	11.4	1.0	15	1	AAV48867	Human GSS gene pol
C 272	12	1.1	13	1	ABC09085	Oligonucleotide SE	C 345	11.4	1.0	15	1	AAV48867	Human GSS gene pol
C 273	12	1.1	13	1	ABC09085	Oligonucleotide SE	C 346	11.4	1.0	15	1	AAV48867	Human focal adhesi
C 274	12	1.1	15	1	AAV48867	Colony stimulating	C 347	11.4	1.0	15	1	AAV48867	Human connexin gen
C 275	12	1.1	15	1	AAV48867	Colony stimulating	C 348	11.4	1.0	15	1	AAV48867	Murine Vrl1 exon la
C 276	12	1.1	15	1	AAV48867	Human PON-1 gene p	C 349	11.4	1.0	15	1	AAV48867	Murine Vrl1 exon la
C 277	12	1.1	15	1	AAV48867	Human PKG2 allele	C 350	11.4	1.0	15	1	AAV48867	Cyp1A1 mRNA detect
C 278	12	1.1	15	1	AAV48867	Murine Cdc25A intr	C 351	11.4	1.0	15	1	AAV48867	Cyp1A1 mRNA detect
C 279	11.8	1.1	17	1	ABK96667	Interleukin-3 (IL-	C 352	11.4	1.0	20	1	AAV48867	PCR primer for hum
C 280	11.8	1.1	15	1	ABK96667	Interleukin-3 (IL-	C 353	11.4	1.0	20	1	AAV48867	RNA component of h
C 281	11.8	1.1	15	1	ABK96667	M. avium 16S rRNA	C 354	11.4	1.0	11	1	AAV48867	RNA component of h
C 282	11.6	1.0	13	1	ABC41583	Oligonucleotide SE	C 355	11.4	1.0	11	1	AAV48867	Human telomerase p
C 283	11.6	1.0	13	1	ABC41583	Oligonucleotide SE	C 356	11.4	1.0	11	1	AAV48867	Human telomerase p
C 284	11.6	1.0	13	1	ABC41583	Oligonucleotide SE	C 357	11.4	1.0	11	1	AAV48867	Human telomerase p
C 285	11.6	1.0	13	1	ABC41582	Oligonucleotide SE	C 358	11.4	1.0	11	1	AAV48867	Human telomerase p
C 286	11.6	1.0	13	1	ABC41582	Oligonucleotide SE	C 359	11.4	1.0	11	1	AAV48867	Human telomerase p
C 287	11.6	1.0	15	1	AAV48867	Colony stimulating	C 360	11.4	1.0	11	1	AAV48867	Human telomerase p
C 288	11.4	1.0	15	1	AAV48867	Colony stimulating	C 361	11.4	1.0	11	1	AAV48867	Human telomerase p
C 289	11.4	1.0	13	1	AAQ52232	Neuroblastoma spec	C 362	11.4	1.0	11	1	AAV48867	Human telomerase p
C 290	11.4	1.0	13	1	AAQ52232	Neuroblastoma spec	C 363	11.4	1.0	11	1	AAV48867	Human skin EST 328
C 291	11.4	1.0	13	1	AAV03419	Enhanced specific	C 364	11.4	1.0	11	1	AAV48867	Human skin EST 774
C 292	11.4	1.0	13	1	AAV03419	Enhanced specific	C 365	11.4	1.0	11	1	AAV48867	Human skin EST 774
C 293	11.4	1.0	13	1	AAV03419	Enhanced specific	C 366	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 294	11.4	1.0	13	1	AAV03419	Enhanced specific	C 367	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 295	11.4	1.0	13	1	AAV03419	Enhanced specific	C 368	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 296	11.4	1.0	13	1	AAV03419	Enhanced specific	C 369	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 297	11.4	1.0	13	1	AAV03419	Enhanced specific	C 370	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 298	11.4	1.0	13	1	AAV03419	Enhanced specific	C 371	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 299	11.4	1.0	13	1	AAV03419	Enhanced specific	C 372	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 300	11.4	1.0	13	1	AAV03419	Enhanced specific	C 373	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 301	11.4	1.0	13	1	AAV03419	Enhanced specific	C 374	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 302	11.4	1.0	13	1	AAV03419	Enhanced specific	C 375	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 303	11.4	1.0	13	1	AAV03419	Enhanced specific	C 376	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 304	11.4	1.0	13	1	AAV03419	Enhanced specific	C 377	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 305	11.4	1.0	13	1	AAV03419	Enhanced specific	C 378	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 306	11.4	1.0	13	1	AAV03419	Enhanced specific	C 379	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 307	11.4	1.0	13	1	AAV03419	Enhanced specific	C 380	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 308	11.4	1.0	13	1	AAV03419	Enhanced specific	C 381	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 309	11.4	1.0	13	1	AAV03419	Enhanced specific	C 382	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 310	11.4	1.0	13	1	AAV03419	Enhanced specific	C 383	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 311	11.4	1.0	13	1	AAV03419	Enhanced specific	C 384	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 312	11.4	1.0	13	1	AAV03419	Enhanced specific	C 385	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 313	11.4	1.0	13	1	AAV03419	Enhanced specific	C 386	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 314	11.4	1.0	13	1	AAV03419	Enhanced specific	C 387	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 315	11.4	1.0	13	1	AAV03419	Enhanced specific	C 388	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 316	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 389	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 317	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 390	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 318	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 391	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 319	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 392	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 320	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 393	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 321	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 394	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 322	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 395	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 323	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 396	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 324	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 397	11.4	1.0	11	1	AAV48867	Oligonucleotide pr
C 325	11.4	1.0	14	1	AAV48867	Erbb-2 gene antis	C 398	11.4	1.0	11	1	AAV48867	Oligonucleotide pr

C 399 11 1.0 12 1 ABH79336 Oligonucleotide pr
C 400 11 1.0 12 1 ABI31168 Oligonucleotide pr
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C 404 11 1.0 12 1 ABH93281 Oligonucleotide pr
C 405 11 1.0 12 1 ABH93281 Oligonucleotide pr
C 406 11 1.0 12 1 ACA62980 Tandem N-box probe
C 407 11 1.0 12 1 ACA62980 Tandem N-box probe
C 408 11 1.0 12 1 ADA00988 Mouse DNA containi
C 409 11 1.0 12 1 ADA00988 Mouse DNA containi
C 410 11 1.0 12 1 ADD10236 GA binding protein
C 411 11 1.0 12 1 ADD10236 GA binding protein
C 412 11 1.0 13 1 ABF4983 Oligonucleotide SE
C 413 11 1.0 13 1 ABF4983 Oligonucleotide SE
C 414 11 1.0 13 1 AAX00290 Target DNA sequenc
C 415 11 1.0 13 1 AAX00290 Target DNA sequenc
C 416 11 1.0 13 1 ABC68546 Oligonucleotide SE
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ALIGNMENTS

RESULT 1
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 ID AAV63648 standard; DNA; 30 BP.
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 AC AAV63648;
 XX
 DT 15-FEB-1999 (first entry)
 XX
 DE Antisense oligonucleotide 13 for human telomerase RNA component.
 XX
 KW Human; telomerase RNA component; anticancer therapy; purification; assay;
 KW vaccine; cancer; antisense oligonucleotide; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
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 XX
 PN WO9845450-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 04-APR-1997; 97WO-US006012.
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 PR 04-APR-1997; 97WO-US006012.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA;
 PI Kealey JT;
 XX
 DR WPI; 1998-594485/50.
 XX
 PT Purification of telomerase on affinity material - useful for, e.g.
 PT diagnosis and treatment of cancer.
 XX
 PS Disclosure; Page 24; 76pp; English.
 XX
 CC The present sequence represents an antisense oligonucleotide directed
 CC against the human telomerase RNA component gene sequences. The
 CC oligonucleotide can be used as an affinity agent in the methods of the
 CC invention, which are used to purify human telomerase. The methods involve
 CC the use of several sequential steps, including the use of two matrices
 CC that bind molecules bearing negative charges, a matrix that binds
 CC molecules bearing positive charges, an affinity purification step and a

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 07:29:59 ; Search time 0.001 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-436-060A-12

Perfect score: 7

Sequence: 1 gctctag 7

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 14 seqs, 114 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 19 summaries

Database : rge12.seq*

Pred. No. is the number of results predicted by chance, to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	1 BD023708	ACCESSION:BD023708
2	7	100.0	9	1 A83648	ACCESSION:A83648
3	7	100.0	9	1 BD106461	ACCESSION:BD106461
4	7	100.0	9	1 S98713	ACCESSION:S98713
5	6	85.7	8	1 BD260031	ACCESSION:BD260031
6	6	85.7	8	1 E13216	ACCESSION:E13216
7	6	85.7	8	1 E17002	ACCESSION:E17002
8	6	85.7	8	1 E17002	ACCESSION:E17002
9	6	85.7	8	1 E17034	ACCESSION:E17034
10	6	85.7	8	1 E17034	ACCESSION:E17034
11	6	85.7	8	1 E17045	ACCESSION:E17045
12	6	85.7	8	1 E17045	ACCESSION:E17045
13	6	85.7	8	1 E1637	ACCESSION:E1637
14	6	85.7	8	1 E1637	ACCESSION:E1637
15	6	85.7	8	1 AX003296	ACCESSION:AX003296
16	6	85.7	8	1 AX687098	ACCESSION:AX687098
17	6	85.7	8	1 AX687099	ACCESSION:AX687099
18	6	85.7	8	1 BD092167	ACCESSION:BD092167
19	6	85.7	8	1 BD092167	ACCESSION:BD092167

ALIGNMENTS

RESULT 1
BD023708
LOCUS BD023708 7 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting and inhibiting RNA component of telomerase.
ACCESSION BD023708
VERSION BD023708.1 GI:22564931
KEYWORDS JP 2001507229-A/12.
SOURCE unidentified
ORGANISM unidentified

unclassified.

1 (bases 1 to 7)

AUTHORS Kim N.W., Wu F., Kealey J.T., Pruzan, R. and Weinrich, S.L.

TITLE Method for detecting and inhibiting RNA component of telomerase

JOURNAL Patent: JP 2001507229-A 12 05-JUN-2001;

COMMENT GERON CORP

PN JP 2001507229-A/12

FD 05-JUN-2001

PF 19-DEC-1997 JP 1998529003

PR 20-DEC-1996 US 08/770564, 20-DEC-1996 US 08/770565 PI

NAM WOO KIM, FRED WU, JAMES T KEALEY, RONALD PRUZAN, SCOTT L PI

WEINRICH

PC C12N15/09, A61K9/08, A61K31/7105, A61K45/00, A61K48/00, A61P35/00,

PC C12N5/10,

PC C12N9/12, C12Q1/68, C12Q1/68, C12N15/00, C12N5/00 CC

Strandedness: Single;

CC Topology: Linear;

CC /note= 'oligo 21ab1'

PH Key Location/Qualifiers.

source 1..7 Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;

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Db 1 GCTCTAG 7

RESULT 2

A83648

LOCUS A83648 9 bp DNA linear PAT 21-JAN-2000

DEFINITION Sequence 4 from Patent WO9849309.

ACCESSION A83648

VERSION A83648.1 GI:6732898

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 9)

Utans-Schneitz, U. and Lesslauer, W.

RAT ST38.2 CHEMOKINE

PATENT: WO 9849309-A 4 05-NOV-1998;

HOFFMANN LA ROCHE (CH)

Location/Qualifiers

source 1..9

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAG 7

Db 1 GCTCTAG 7

RESULT 3

BD106461

LOCUS BD106461 9 bp DNA linear PAT 18-SEP-2002

DEFINITION Rat ST38.2 chemokine.

ACCESSION BD106461

VERSION BD106461.1 GI:23201279

KEYWORDS JP 2002500509-A/2.

SOURCE Chlamydia sp.

ORGANISM Chlamydia sp.

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 12:41:14 ; Search time 1 Seconds
(without alignments)

6.384 Million cell updates/sec

Title: frag1-16

Perfect score: 1122

Sequence: 1 cgtctctctctctgagcct.....aggccgcggaaggaagc 1122

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 153 seqs, 2845 residues

Total number of hits satisfying chosen parameters: 306

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 306 summaries

Database : rge1-16.seq *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 38	26	2.3	26	1	AR161925
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C 41	26	2.3	26	1	E37046
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C 105	26	2.3	26	1	AR393335
C 106	26	2.3	26	1	AR393335

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:40:30 ; Search time 0.001 seconds
(without alignments)
46.400 Million cell updates/sec

Title: US-09-436-060A-3

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 112 seqs, 1160 residues

Total number of hits satisfying chosen parameters: 224

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Lining first 112 summaries

Database : rni3.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	11	55.0	11	1	US-08-619-542B-5
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9	11	55.0	12	1	US-08-126-594-6
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12	11	55.0	14	1	US-08-294-424-33
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:36:28 ; Search time 0.001 Seconds
(without alignments)
61.920 Million cell updates/sec

Title: US-09-436-060A-3

Perfect score: 20

Sequence: 1 cgttccttccttcg99cct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 135 seqs, 1548 residues

Total number of hits satisfying chosen parameters: 270

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 135 summaries

Database : rge3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model

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17.760 Million cell updates/sec

Title: US-09-436-060A-4
Perfect score: 12
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Scoring table: IDENTITY NUC
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Searched: 81 seqs, 740 residues

Total number of hits satisfying chosen parameters: 162

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
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Listing first 81 summaries

Database : rnpb4.seq.*

Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Publication No. US20030044392A1
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; APPLICANT: Hung, Men-Chie
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; FILE REFERENCE: UTS-582
; CURRENT APPLICATION NUMBER: US/09/884.363
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/116,049
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
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; TYPE: DNA
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US-09-884-363-10

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:51:03 ; Search time 1 Seconds
(without alignments)
0.017 Million cell updates/sec

Title: US-09-436-060A-4

Perfect score: 12

Sequence: 1 cgtctctcttc 12

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 83 seqs, 714 residues

Total number of hits satisfying chosen parameters: 166

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 83 summaries

Database : rni4.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	12	100.0	12	1	US-08-770-565-4
2	9	75.0	10	1	Sequence 4, Appli
3	9	75.0	10	1	Sequence 8, Appli
4	9	75.0	10	1	Sequence 8, Appli
5	9	75.0	10	1	Sequence 10, Appl
6	9	75.0	10	1	Sequence 27, Appl
7	9	75.0	10	1	Sequence 10, Appl
8	8.4	70.0	10	1	Sequence 13, Appl
9	8.4	70.0	10	1	Sequence 103, App
10	8.4	70.0	10	1	Sequence 203, App
11	8.4	70.0	10	1	Sequence 225, App
12	8	66.7	8	1	Sequence 262, App
13	8	66.7	10	1	Sequence 48, Appl
14	8	66.7	10	1	Sequence 48, Appl
15	8	66.7	10	1	Sequence 137, App
16	8	66.7	10	1	Sequence 656, App
17	8	66.7	10	1	Sequence 656, App
18	8	66.7	10	1	Sequence 188, App
19	8	66.7	10	1	Sequence 190, App
20	8	66.7	10	1	Sequence 188, App
21	8	66.7	10	1	Sequence 188, App
22	8	66.7	10	1	Sequence 11, Appl
23	8	66.7	10	1	Sequence 137, App
24	8	66.7	10	1	Sequence 656, App
25	8	66.7	10	1	Sequence 16, Appl
26	8	66.7	10	1	Sequence 137, App
27	8	66.7	10	1	Sequence 137, App
28	7	58.3	7	1	Sequence 10, Appl
29	7	58.3	7	1	Sequence 187, App
30	7	58.3	7	1	Sequence 261, App
31	7	58.3	7	1	Sequence 309, App
32	7	58.3	7	1	Sequence 126, App
33	7	58.3	7	1	Sequence 126, App

C 34	7	58.3	9	1	US-08-711-417C-126	Sequence 126, App
C 35	7	58.3	9	1	US-09-723-909-126	Sequence 126, App
C 36	7	58.3	9	1	PCT-US93-08743-126	Sequence 126, App
C 37	6.4	53.3	8	1	US-08-187-749-6	Sequence 2, Appli
C 38	6.4	53.3	8	1	US-08-662-963-2	Sequence 3, Appli
C 39	6.4	53.3	8	1	US-08-662-963-3	Sequence 3, Appli
C 40	6.4	53.3	8	1	US-08-662-963-10	Sequence 10, Appl
C 41	6.4	53.3	8	1	US-08-662-963-16	Sequence 16, Appl
C 42	6.4	53.3	8	1	US-08-662-963-18	Sequence 18, Appl
C 43	6.4	53.3	8	1	US-08-488-015B-15	Sequence 15, Appl
C 44	6.4	53.3	8	1	US-08-859-954-242	Sequence 242, App
C 45	6.4	53.3	8	1	US-08-859-954-551	Sequence 551, App
C 46	6.4	53.3	8	1	US-09-585-599A-3	Sequence 3, Appli
C 47	6.4	53.3	8	1	US-04-585-599A-5	Sequence 5, Appli
C 48	6.4	53.3	8	1	US-09-835-370-64	Sequence 64, Appl
C 49	6.4	53.3	8	1	PCT-US95-01104-6	Sequence 6, Appli
C 50	6.2	51.7	7	1	US-08-488-015B-21	Sequence 21, Appl
C 51	6	50.0	7	1	US-07-630-288A-9	Sequence 9, Appli
C 52	6	50.0	7	1	US-08-468-049-9	Sequence 9, Appli
C 53	6	50.0	7	1	US-08-855-372B-44	Sequence 44, Appl
C 54	6	50.0	7	1	US-08-855-372B-45	Sequence 45, Appl
C 55	6	50.0	7	1	US-08-855-372B-68	Sequence 68, Appl
C 56	6	50.0	7	1	US-08-855-372B-69	Sequence 69, Appl
C 57	6	50.0	7	1	US-09-498-851-44	Sequence 44, Appl
C 58	6	50.0	7	1	US-09-498-851-45	Sequence 45, Appl
C 59	6	50.0	7	1	US-09-498-851-68	Sequence 68, Appl
C 60	6	50.0	7	1	US-09-498-851-69	Sequence 69, Appl
C 61	6	50.0	7	1	US-09-328-925-2	Sequence 2, Appli
C 62	6	50.0	8	1	US-08-509-858-3	Sequence 3, Appli
C 63	6	50.0	8	1	US-08-465-590-135	Sequence 135, App
C 64	6	50.0	8	1	US-08-227-180B-4	Sequence 4, Appli
C 65	6	50.0	8	1	US-08-227-180B-5	Sequence 5, Appli
C 66	6	50.0	8	1	US-08-859-954-129	Sequence 129, App
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C 68	6	50.0	8	1	US-08-859-954-263	Sequence 263, App
C 69	6	50.0	8	1	US-08-859-954-264	Sequence 264, App
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C 71	6	50.0	8	1	US-08-859-954-354	Sequence 354, App
C 72	6	50.0	8	1	US-08-859-954-434	Sequence 434, App
C 73	6	50.0	8	1	US-08-859-954-482	Sequence 482, App
C 74	6	50.0	8	1	US-08-859-954-483	Sequence 483, App
C 75	6	50.0	8	1	US-08-859-954-488	Sequence 488, App
C 76	6	50.0	8	1	US-08-859-954-518	Sequence 518, App
C 77	6	50.0	8	1	US-08-859-954-559	Sequence 559, App
C 78	6	50.0	8	1	US-09-063-450-13	Sequence 13, Appl
C 79	6	50.0	8	1	US-08-711-417C-135	Sequence 135, App
C 80	6	50.0	8	1	US-09-723-909-135	Sequence 135, App
C 81	6	50.0	8	1	US-09-682-562-1	Sequence 1, Appli
C 82	6	50.0	8	1	US-09-682-562-3	Sequence 3, Appli
C 83	6	50.0	8	1	PCT-US93-08743-135	Sequence 135, App

ALIGNMENTS

RESULT 1
US-08-770-565-4
; Sequence 4, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:49:39 ; Search time 1 Seconds

(without alignments)
0.038 Million cell updates/sec

Title: US-09-436-060A-4

Perfect score: 12

Sequence: 1 cgtctctcttc 12

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 160 seqs, 1603 residues

Total number of hits satisfying chosen parameters: 320

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 160 summaries

Database : rng4.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	10	83.3	12	1 AB117903	Oligonucleotide pr
4	10	83.3	12	1 AC642980	Tandem N-box probe
5	10	83.3	12	1 ADA00988	Mouse DNA containi
6	10	83.3	12	1 ADQ10236	GA binding protein
7	9.4	78.3	11	1 ABV68239	Human skin EST 602
8	9.4	78.3	11	1 ADQ32773	Human hair-bearing
9	9.4	78.3	11	1 AB128525	Human facial skin-
10	9.4	78.3	12	1 AB123385	Oligonucleotide pr
11	9.4	78.3	12	1 AB103041	Oligonucleotide pr
12	9.4	78.3	12	1 AB128526	Oligonucleotide pr
13	9.4	78.3	12	1 ABH69570	Oligonucleotide pr
14	9.4	78.3	12	1 AAZ50022	SV40 enhancer for
15	9	75.0	10	1 AAF43218	Yeast NORF gene SA
16	9	75.0	10	1 AAO37031	NF-AT complex bind
17	9	75.0	12	1 AAX54574	Human IGE receptor
18	9	75.0	12	1 ABF21434	Human IGE receptor
19	9	75.0	12	1 ABF19924	Oligonucleotide pr
20	9	75.0	12	1 AB111122	Oligonucleotide pr
21	9	75.0	12	1 ABH80463	Oligonucleotide pr
22	9	75.0	12	1 ABH86427	Oligonucleotide pr
23	9	75.0	12	1 ABH77320	Oligonucleotide pr
24	9	75.0	12	1 AB124917	Oligonucleotide pr
25	9	75.0	12	1 ABH74926	Oligonucleotide pr
26	9	75.0	12	1 ABH7651	Oligonucleotide pr
27	9	75.0	12	1 ABH70318	Oligonucleotide pr
28	9	75.0	12	1 ABH6296	Oligonucleotide pr
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C 38	8.4	70.0	10	1 AAX14766	Triple helix formi
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C 40	8.4	70.0	10	1 AAZ83081	Metastatic breast
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C 51	8.4	70.0	10	1 ACD06060	Human VEGF-targete
C 52	8.4	70.0	10	1 ACD19282	Human CERP gene a
C 53	8.4	70.0	10	1 ADG98629	Human VEGF-targete
C 54	8.4	70.0	10	1 ADL33591	DNA binding protei
C 55	8.4	70.0	10	1 ADM72632	DNA sequence of tar
C 56	8.4	70.0	11	1 AAX14838	Triple helix formi
C 57	8.4	70.0	11	1 ABV67129	Human skin EST 491
C 58	8.4	70.0	11	1 ABV67709	Human skin EST 549
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C 61	8.4	70.0	11	1 ABV70293	Human skin EST 405
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C 64	8	66.7	9	1 ABQ71419	A. thaliana primer
C 65	8	66.7	9	1 ABQ71418	Zinc finger protei
C 66	8	66.7	9	1 ADA62567	Zinc finger protei
C 67	8	66.7	9	1 ADA62566	Zinc finger target
C 68	8	66.7	9	1 ADM30770	Synthetic zinc fin
C 69	8	66.7	9	1 ADM30771	Synthetic zinc fin
C 70	8	66.7	10	1 AAG61538	IL2 PuBp enhancer
C 71	8	66.7	10	1 AAQ96592	HIV-1 NL4-3 nef ge
C 72	8	66.7	10	1 AAQ96593	HIV-1 NL4-3 nef ge
C 73	8	66.7	10	1 AAQ96594	HIV-1 NL4-3 nef ge
C 74	8	66.7	10	1 AAV45395	5'-primer for mam
C 75	8	66.7	10	1 AAV45395	PuBp binding site
C 76	8	66.7	10	1 AAV67094	IL2 enhancer PuBp.
C 77	8	66.7	10	1 AAV50139	Yeast tag for NORF
C 78	8	66.7	10	1 AAX17656	PNA-thiazole orang
C 79	8	66.7	10	1 AAX17656	Bis-distamycin tar
C 80	8	66.7	10	1 AAZ78579	Human dendritic ce
C 81	8	66.7	10	1 AAZ78286	Human dendritic ce
C 82	8	66.7	10	1 AAZ81452	Metastatic breast
C 83	8	66.7	10	1 AAZ84987	Metastatic breast
C 84	8	66.7	10	1 AAZ83001	Metastatic breast
C 85	8	66.7	10	1 AAF33370	Yeast NORF gene SA
C 86	8	66.7	10	1 AAF33640	Yeast NORF gene SA
C 87	8	66.7	10	1 AAF33356	Yeast NORF gene SA
C 88	8	66.7	10	1 AAF3381	Yeast NORF gene SA
C 89	8	66.7	10	1 AAF34913	Yeast NORF gene SA
C 90	8	66.7	10	1 AAF39588	Yeast NORF gene SA
C 91	8	66.7	10	1 ABK68703	Human SCV2 Gene a
C 92	8	66.7	10	1 ABK95861	Solute Carrier Fam
C 93	8	66.7	10	1 ABK83147	DNA binding molecu
C 94	8	66.7	10	1 ABL52311	Human CCR6 prefer
C 95	8	66.7	10	1 ABQ71667	Zinc finger protei
C 96	8	66.7	10	1 ABQ71671	Zinc finger protei
C 97	8	66.7	10	1 AAD43427	Human CYP3A5 gene
C 98	8	66.7	10	1 AAL40868	Zinc finger protei
C 99	8	66.7	10	1 AAL41867	Human GNT1 allele
C 100	8	66.7	10	1 ABH85907	Gamma tocopherol m
C 101	8	66.7	10	1 ABT14371	Nucleic acid PCR a
C 102	8	66.7	10	1 ADA63692	Zinc finger target
C 103	8	66.7	10	1 ADA63688	Zinc finger target
C 104	8	66.7	10	1 ADJ78763	Arabidopsis gamma-
C 105	8	66.7	10	1 ADM22190	Synthetic zinc fin
C 106	8	66.7	10	1 ADM22186	Synthetic zinc fin

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:47:56 ; Search time 0.001 Seconds
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15.144 Million cell updates/sec

Title: US-09-436-060A-4
Perfect score: 12
Sequence: 1 cgtctctcttc 12

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 0.5

Searched: 65 seqs, 631 residues

Total number of hits satisfying chosen parameters: 130

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : rge4.seq *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	1	AR063828
2	12	100.0	12	1	BD023700
3	9.4	78.3	11	1	AR063828
4	9.4	78.3	11	1	AR063828
5	9.4	78.3	11	1	AR063828
6	9.4	78.3	11	1	AR063828
7	9.4	78.3	11	1	AR063828
8	9.4	78.3	11	1	AR063828
9	9.4	78.3	11	1	AR063828
10	9.4	78.3	11	1	AR063828
11	9.4	78.3	11	1	AR063828
12	9.4	78.3	11	1	AR063828
13	9.4	78.3	11	1	AR063828
14	9.4	78.3	11	1	AR063828
15	9.4	78.3	11	1	AR063828
16	9.4	78.3	11	1	AR063828
17	9.4	78.3	11	1	AR063828
18	9.4	78.3	11	1	AR063828
19	9.4	78.3	11	1	AR063828
20	9.4	78.3	11	1	AR063828
21	9.4	78.3	11	1	AR063828
22	9.4	78.3	11	1	AR063828
23	9.4	78.3	11	1	AR063828
24	9.4	78.3	11	1	AR063828
25	9.4	78.3	11	1	AR063828
26	9.4	78.3	11	1	AR063828
27	9.4	78.3	11	1	AR063828
28	9.4	78.3	11	1	AR063828
29	9.4	78.3	11	1	AR063828
30	9.4	78.3	11	1	AR063828
31	9.4	78.3	11	1	AR063828
32	9.4	78.3	11	1	AR063828
33	9.4	78.3	11	1	AR063828

34	8	66.7	10	1	AR209708
35	8	66.7	10	1	AR236019
36	8	66.7	10	1	AR351850
37	8	66.7	10	1	AR351854
38	8	66.7	10	1	AR404849
39	8	66.7	10	1	AR668210
40	8	66.7	10	1	AR668214
41	8	66.7	10	1	BD065159
42	7.4	61.7	9	1	AR667139
43	7.4	61.7	9	1	AR668586
44	7.4	61.7	9	1	AR668770
45	7.4	61.7	9	1	AR668831
46	7.4	61.7	9	1	AR668978
47	7.4	61.7	9	1	AR668979
48	7.4	61.7	9	1	AR668980
49	7.4	61.7	9	1	AR669025
50	7.4	61.7	9	1	AR669062
51	7.4	61.7	9	1	AR669084
52	7.4	61.7	9	1	AR668885
53	7.4	61.7	9	1	AR668886
54	7.4	61.7	9	1	AR668900
55	6.4	53.3	8	1	AR668927
56	6.4	53.3	8	1	AR668927
57	6.4	53.3	8	1	AR668927
58	6.4	53.3	8	1	AR668927
59	6.4	53.3	8	1	AR668927
60	6.4	53.3	8	1	AR668927
61	6.4	53.3	8	1	AR668927
62	6.4	53.3	8	1	AR668927
63	6.4	53.3	8	1	AR668927
64	6.4	53.3	8	1	AR668927
65	6.4	53.3	8	1	AR668927

ALIGNMENTS

RESULT 1	AR063828	12 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063828	Sequence 4 from patent US 5846723.			
DEFINITION	AR063828				
VERSION	AR063828.1	GI:5993136			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 12)				
AUTHORS	Kim N.Woo., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.				
TITLE	Methods for detecting the RNA component of telomerase				
JOURNAL	Patent: US 5846723-A 4 08-DEC-1998;				
FEATURES	Location/Qualifiers				
source	1..12				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	100.0%; Score 12; DB 1; Length 12;				
Best Local Similarity	100.0%; Pred. No. 3.1;				
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 CGTCTCTCTTC 12				
	1 CGTCTCTCTTC 12				
Db					
RESULT 2	BD023700	12 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD023700	Method for detecting and inhibiting RNA component of telomerase.			
DEFINITION	BD023700				
VERSION	BD023700.1	GI:22564923			
KEYWORDS	JP 2001507229-A/4.				
SOURCE	unidentified				

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:03:59 ; Search time 1 Seconds
(without alignments)
0.014 Million cell updates/sec

Title: US-09-436-060A-6
Perfect score: 20
Sequence: 1 ctgacagagcccaactcttc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 36 seqs, 361 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 36 summaries

Database : rnpb6.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	19	1	US-10-093-958-22
2	9	45.0	10	1	US-10-033-145-87
3	9	45.0	10	1	US-10-033-145-1959
4	9	45.0	10	1	US-10-398-877-25
5	8.4	42.0	10	1	US-03-184-750A-53
6	8.4	42.0	10	1	US-03-989-789-1273
7	8.4	42.0	10	1	US-03-990-186-1273
8	8.4	42.0	10	1	US-03-748-710-31
9	8.4	42.0	10	1	US-03-989-994-1273
10	8.4	42.0	10	1	US-10-033-145-480
11	8.4	42.0	10	1	US-10-330-627-1329
12	8.4	42.0	10	1	US-10-330-627-1330
13	8.4	42.0	10	1	US-03-249-155-220
14	8.4	42.0	10	1	US-10-314-322-220
15	8.4	42.0	10	1	US-10-199-762B-8
16	8.4	42.0	10	1	US-10-450-797-119
17	8.4	42.0	10	1	US-10-450-797-1131
18	8	40.0	9	1	US-03-916-466-213
19	8	40.0	9	1	US-10-277-494-213
20	8	40.0	10	1	US-10-033-145-237
21	8	40.0	10	1	US-10-033-145-2010
22	8	40.0	10	1	US-10-033-145-2100
23	8	40.0	10	1	US-10-176-464A-41
24	8	40.0	10	1	US-10-231-765-235
25	8	40.0	10	1	US-10-330-627-1165
26	7.4	37.0	9	1	US-03-989-789-2433
27	7.4	37.0	9	1	US-03-989-789-2449
28	7.4	37.0	9	1	US-03-916-466-212
29	7.4	37.0	9	1	US-03-990-186-2433
30	7.4	37.0	9	1	US-03-990-186-2449
31	7.4	37.0	9	1	US-03-989-994-2433
32	7.4	37.0	9	1	US-03-989-994-2449
33	7.4	37.0	9	1	US-10-059-579-125

ALIGNMENTS

RESULT 1

US-10-093-958-22
; Sequence 22, Application US/10093958
; Publication No. US20030044423A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Jeffrey, Way
; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
; FILE REFERENCE: MOIETY
; CURRENT APPLICATION NUMBER: US/10/093,958
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,096
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: forward primer for gamma 1 hinge region
US-10-093-958-22

Query Match 72.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTC 20

DB 4 CAGAGCCCAACTCTTC 19

RESULT 2

US-10-033-145-87/c
; Sequence 87, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAC201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 87
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-87

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCA 13

DB 9 CAGAGCCCA 1

RESULT 3

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:01:36 ; Search time 0.001 Seconds
(without alignments)
8.400 Million cell updates/sec

Title: US-09-436-060A-6

Perfect score: 20

Sequence: .. 1 ctgacagagcccaactcttc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 21 seqs, 210 residues

Total number of hits satisfying chosen parameters: 42

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 21 summaries

Database : rni6.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	20	100.0	20	1	US-08-770-565-6
2	12.4	62.0	15	1	US-08-311-486C-658
3	9	45.0	12	1	US-09-508-753B-472
4	8.4	42.0	10	1	US-08-388-353-191
5	8.4	42.0	10	1	US-08-388-353-192
6	8.4	42.0	10	1	US-08-488-551B-191
7	8.4	42.0	10	1	US-08-488-551B-192
8	8.4	42.0	10	1	US-09-154-750A-53
9	8.4	42.0	11	1	US-09-249-155A-220
10	8	40.0	8	1	US-08-859-954-300
11	8	40.0	10	1	US-08-171-718-21
12	8	40.0	10	1	US-08-478-087-21
13	7.4	37.0	9	1	PCT-US91-03680-137
14	7	35.0	8	1	US-08-859-954-224
15	7	35.0	8	1	US-08-859-954-226
16	7	35.0	8	1	US-08-859-954-281
17	7	35.0	8	1	US-08-859-954-458
18	7	35.0	8	1	US-08-859-954-463
19	7	35.0	8	1	US-09-063-450-4
20	7	35.0	8	1	US-09-781-697-3
21	6.8	34.0	9	1	PCT-US91-03680-139

ALIGNMENTS

RESULT 1
US-08-770-565-6
; Sequence 6, Application US/0870565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-6

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20
Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2
US-08-311-486C-658
; Sequence 658, Application US/08311486C
; Patent No. 5811360
; GENERAL INFORMATION:
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth Draper
; APPLICANT: Kevin Kisich
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwigen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2086
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:58:14 ; Search time 0.001 Seconds
(without alignments)
30.680 Million cell updates/sec

Title: US-09-436-060A-6
Perfect score: 20
Sequence: 1 CTGACAGAGCCCAACTCTTC 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 70 seqs, 767 residues

Total number of hits satisfying chosen parameters: 140

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database: rge6.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1	AR063830
2	20	100.0	20	1	BD023702
3	12.4	62.0	15	1	AR041868
4	12.4	62.0	15	1	AR037286
5	11	55.0	12	1	AI4857
6	10.8	54.0	14	1	AX040869
7	9.4	47.0	11	1	AX627809
8	9.4	47.0	11	1	AX629164
9	9	45.0	10	1	BD238669
10	9	45.0	10	1	BD240541
11	9	45.0	10	1	BD168118
12	9	45.0	11	1	CQ828612
13	9	45.0	11	1	CQ832855
14	9	45.0	11	1	CQ835054
15	9	45.0	11	1	CQ836871
16	9	45.0	11	1	CQ837830
17	9	45.0	11	1	AX625389
18	9	45.0	11	1	AX629494
19	9	45.0	12	1	AR303747
20	8.4	42.0	10	1	BD239062
21	8.4	42.0	10	1	E54681
22	8.4	42.0	10	1	AR223000
23	8.4	42.0	10	1	AR351731
24	8.4	42.0	10	1	AX153414
25	8.4	42.0	10	1	AX153415
26	8.4	42.0	10	1	AX189813
27	8.4	42.0	10	1	AX667824
28	8.4	42.0	10	1	BD083143
29	8.4	42.0	10	1	BD083183
30	8.4	42.0	10	1	BD091175
31	8.4	42.0	10	1	BD166802
32	8.4	42.0	10	1	BD167087
33	8.4	42.0	11	1	CQ779556

C	34	8.4	42.0	11	1	CQ832917
	35	8.4	42.0	11	1	AR035667
	36	8.4	42.0	11	1	CQ835753
	37	8.4	42.0	11	1	CQ836179
	38	8.4	42.0	11	1	CQ836439
	39	8.4	42.0	11	1	CQ837276
	40	8.4	42.0	11	1	CQ837532
	41	8.4	42.0	11	1	CQ837623
	42	8.4	42.0	11	1	AR301639
	43	8.4	42.0	11	1	AX099093
	44	8.4	42.0	11	1	AX099094
	45	8.4	42.0	11	1	AX470542
	46	8.4	42.0	11	1	AX471554
	47	8.4	42.0	11	1	AX623315
	48	8.4	42.0	11	1	AX623791
	49	8.4	42.0	11	1	AX626314
	50	8.4	42.0	11	1	AX627234
	51	8.4	42.0	11	1	AX627767
	52	8.4	42.0	11	1	AX627978
	53	8.4	42.0	11	1	AX627980
	54	8.4	42.0	11	1	AX628396
	55	8.4	42.0	11	1	AX630286
	56	8.4	42.0	11	1	AX630736
	57	8.4	42.0	11	1	AX631212
	58	8.4	42.0	11	1	BD124389
	59	8	40.0	10	1	AR098885
	60	8	40.0	10	1	BD238819
	61	8	40.0	10	1	BD240592
	62	8	40.0	10	1	BD240682
	63	8	40.0	10	1	I79725
	64	8	40.0	10	1	AX153250
	65	8	40.0	10	1	BD161413
	66	8	40.0	10	1	BD166512
	67	7.6	38.0	8	1	E25503
	68	7.6	38.0	8	1	E25506
	69	7.4	37.0	9	1	AX668984
	70	7.4	37.0	9	1	AX669000

ALIGNMENTS

RESULT 1	AR063830	20 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 6 from patent US 5846723.				
DEFINITION	AR063830				
ACCESSION	AR063830.1				
VERSION	GI:5993138				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.				
TITLE	Methods for detecting the RNA component of telomerase				
JOURNAL	Patent: US 5846723-A 6 08-DEC-1998;				
FEATURES	Location/Qualifiers				
	1..20				
	/organism="unknown"				
	/mol_type="unassigned DNA"				

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACAGAGCCCAACTCTTC 20

Db 1 CTGACAGAGCCCAACTCTTC 20

RESULT 2

BD023702

LOCUS 20 bp DNA linear PAT 27-AUG-2002

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	20	100.0	20	1	AAV41174	RNA component of h
C 2	16	80.0	21	1	ADP93861	Human TERR siRNA,
C 3	16	80.0	21	1	ADG30030	hTR-targeted siNA
C 4	11	55.0	12	1	AI41062	Oligonucleotide pr
C 5	11	55.0	13	1	AAU00290	Target DNA sequenc
C 6	10.4	52.0	12	1	AI19475	Oligonucleotide pr
C 7	10.4	52.0	13	1	AAU00297	Target DNA sequenc
C 8	10.4	52.0	13	1	ABC70351	Oligonucleotide SE
C 9	10.4	52.0	13	1	ABC70350	Oligonucleotide SE
C 10	10.4	52.0	13	1	AB297740	Oligonucleotide SE
C 11	10.4	52.0	13	1	AB297741	Oligonucleotide SE
C 12	10	50.0	10	1	AAFA0580	Oligonucleotide SE
C 13	10	50.0	12	1	AB154849	Yeast NORF gene SA
C 14	10	50.0	12	1	AB142091	Oligonucleotide pr
C 15	10	50.0	12	1	AB181242	Oligonucleotide pr
C 16	10	50.0	13	1	AB17515	Oligonucleotide pr
C 17	10	50.0	13	1	AB17515	Oligonucleotide SE
C 18	10	50.0	13	1	ABFA7778	Oligonucleotide SE
C 19	10	50.0	13	1	ABH33141	Oligonucleotide SE
C 20	10	50.0	13	1	ABFA7779	Oligonucleotide SE
C 21	10	50.0	13	1	ABH33140	Oligonucleotide SE
C 22	9.4	47.0	11	1	ABG17514	Oligonucleotide SE
C 23	9.4	47.0	12	1	ABV68750	Oligonucleotide SE
C 24	9.4	47.0	12	1	AB138049	Human skin ESR 653
C 25	9.4	47.0	12	1	AB125442	Oligonucleotide pr
C 26	9.4	47.0	12	1	AB141061	Oligonucleotide pr
C 27	9.4	47.0	12	1	AB115215	Oligonucleotide pr
C 28	9.4	47.0	12	1	AB108643	Oligonucleotide pr
C 29	9	45.0	10	1	AB107158	Oligonucleotide pr
C 30	9	45.0	10	1	AAV34959	Oligonucleotide pr
C 31	9	45.0	10	1	AAV50086	Synthetic Agaricus
C 32	9	45.0	10	1	AAV283525	Yeast tag for puta
C 33	9	45.0	10	1	AAV33303	Metastatic breast
C 34	9	45.0	10	1	AAV33303	Yeast putative cod
C 35	9	45.0	10	1	AAFA1954	Yeast NORF gene SA

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:11:16 ; Search time 0.001 Seconds
(without alignments)
25.360 Million cell updates/sec

Title: US-09-436-060A-7

Perfect score: 20

Sequence: 1 ccaactcttcgcggtggcag 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 60 seqs, 634 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database : rge7.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1	AR063831
2	20	100.0	20	1	BD023703
C 3	10.8	54.0	14	1	AR9176
C 4	10.8	54.0	14	1	BD066689
C 5	10	50.0	11	1	118772
C 6	10	50.0	11	1	195608
7	9.4	47.0	11	1	AX629495
8	9	45.0	10	1	BD065106
C 9	8.4	42.0	10	1	BD168118
C 10	8.4	42.0	10	1	ES4735
11	8.4	42.0	10	1	AR351835
12	8.4	42.0	10	1	AR351836
C 13	8.4	42.0	10	1	AX152445
C 14	8.4	42.0	10	1	AX377146
15	8.4	42.0	10	1	AX668192
16	8.4	42.0	10	1	AX668191
C 17	8.4	42.0	10	1	AX814791
C 18	8.4	42.0	10	1	BD065323
C 19	8.4	42.0	10	1	BD167133
C 20	8.4	42.0	10	1	BD167245
21	8.4	42.0	11	1	CQ833209
C 22	8.4	42.0	11	1	CQ836219
C 23	8.4	42.0	11	1	AX471580
C 24	8.4	42.0	11	1	AX626651
C 25	8.4	42.0	11	1	AX628423
C 26	8.4	42.0	11	1	AX628485
27	8.4	42.0	11	1	AX629184
28	8	40.0	9	1	AX668855
29	8	40.0	9	1	AX668856
30	8	40.0	10	1	AR026407
31	8	40.0	10	1	AR052583
C 32	8	40.0	10	1	BD238745
33	8	40.0	10	1	BD238911

C 34	8	40.0	10	1	E39527
C 35	8	40.0	10	1	E39571
C 36	8	40.0	10	1	I34894
37	8	40.0	10	1	I83515
38	8	40.0	10	1	AR351805
39	8	40.0	10	1	AR351839
40	8	40.0	10	1	AR351855
41	8	40.0	10	1	AR351863
42	8	40.0	10	1	AR351866
43	8	40.0	10	1	AR351883
44	8	40.0	10	1	AR351884
45	8	40.0	10	1	AR473558
46	8	40.0	10	1	AX214428
47	8	40.0	10	1	AX320713
48	8	40.0	10	1	AX668156
49	8	40.0	10	1	AX668195
50	8	40.0	10	1	AX668215
51	8	40.0	10	1	AX668223
52	8	40.0	10	1	AX668226
53	8	40.0	10	1	AX668243
54	8	40.0	10	1	AX668244
C 55	8	40.0	10	1	BD007856
C 56	8	40.0	10	1	BD083291
57	8	40.0	10	1	BD166512
C 58	8	40.0	10	1	S75141
C 59	7.4	37.0	9	1	AX665471
C 60	7.4	37.0	9	1	BD069703

ALIGNMENTS

RESULT 1	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
ACCESSION	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
VERSION	AR063831.1	GI:5993139	20 bp	DNA	linear	PAT 29-SEP-1999
KEYWORDS	AR063831.1	GI:5993139	20 bp	DNA	linear	PAT 29-SEP-1999
SOURCE	Unknown.	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
ORGANISM	Unknown.	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
REFERENCE	1 (bases 1 to 20)	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
AUTHORS	Kim, N.W., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
TITLE	Methods for detecting the RNA component of telomerase	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
JOURNAL	Patent: US 5846723-A 7 08-DEC-1998;	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
FEATURES	Location/Qualifiers	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
source	1..20	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
	/organism="unknown"	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
	/mol_type="unassigned DNA"	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCAACTCTTCGCGTGGCAG 20
Db 1 CCAACTCTTCGCGTGGCAG 20

RESULT 2	BD023703	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD023703	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	BD023703	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
ACCESSION	BD023703	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
VERSION	BD023703.1	GI:22564926	20 bp	DNA	linear	PAT 27-AUG-2002
KEYWORDS	JP 2001507229-A/7.	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
SOURCE	unidentified	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
ORGANISM	unclassified.	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
REFERENCE	1 (bases 1 to 20)	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
AUTHORS	Kim, N.W., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
TITLE	Method for detecting and inhibiting RNA component of telomerase	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:26:22 ; Search time 0.001 Seconds
(without alignments)
22.840 Million cell updates/sec

Title: US-09-436-060A-7

Perfect score: 20

Sequence: 1 ccaactcttcggtgagcag 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 56 seqs, 571 residues

Total number of hits satisfying chosen parameters: 112

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 56 summaries

Database : rnpb7.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9.8	49.0	13	1	US-09-864-636A-1062
2	9.8	49.0	13	1	US-09-864-636A-1187
3	9.8	49.0	13	1	US-09-864-426A-1062
4	9.8	49.0	13	1	US-09-864-426A-1187
5	9.8	49.0	13	1	US-10-084-839-1062
6	9.8	49.0	13	1	US-10-084-839-1187
7	9	45.0	10	1	US-10-398-877-25
8	9	45.0	11	1	US-09-836-737A-4
9	8.4	42.0	10	1	US-09-989-789-1640
10	8.4	42.0	10	1	US-09-989-789-1641
11	8.4	42.0	10	1	US-09-989-789-1640
12	8.4	42.0	10	1	US-09-990-186-1640
13	8.4	42.0	10	1	US-09-990-186-1641
14	8.4	42.0	10	1	US-09-989-994-1640
15	8.4	42.0	10	1	US-09-989-994-1641
16	8.4	42.0	10	1	US-10-329-463-70
17	8.4	42.0	10	1	US-10-330-627-360
18	8.4	42.0	11	1	US-10-356-792-37
19	8	40.0	9	1	US-10-450-797-1157
20	8	40.0	9	1	US-09-989-789-2304
21	8	40.0	9	1	US-09-989-789-2305
22	8	40.0	9	1	US-09-916-468-174
23	8	40.0	9	1	US-09-990-186-2304
24	8	40.0	9	1	US-09-990-186-2305
25	8	40.0	9	1	US-09-989-994-2304
26	8	40.0	9	1	US-09-989-994-2305
27	8	40.0	9	1	US-10-277-494-174
28	8	40.0	10	1	US-09-779-233-36
29	8	40.0	10	1	US-09-989-789-1605
30	8	40.0	10	1	US-09-989-789-1644
31	8	40.0	10	1	US-09-989-789-1664
32	8	40.0	10	1	US-09-989-789-1672
33	8	40.0	10	1	US-09-989-789-1675

34	8	40.0	10	1	US-09-989-789-1693
35	8	40.0	10	1	US-09-844-508-44
36	8	40.0	10	1	US-09-990-186-1605
37	8	40.0	10	1	US-09-990-186-1644
38	8	40.0	10	1	US-09-990-186-1664
39	8	40.0	10	1	US-09-990-186-1672
40	8	40.0	10	1	US-09-990-186-1693
41	8	40.0	10	1	US-09-990-186-1693
42	8	40.0	10	1	US-09-989-994-1605
43	8	40.0	10	1	US-09-989-994-1644
44	8	40.0	10	1	US-09-989-994-1664
45	8	40.0	10	1	US-09-989-994-1672
46	8	40.0	10	1	US-09-989-994-1693
47	8	40.0	10	1	US-09-989-994-1693
48	8	40.0	10	1	US-09-989-994-1693
49	8	40.0	10	1	US-09-989-994-1693
50	8	40.0	10	1	US-10-033-145-329
51	8	40.0	10	1	US-10-033-145-329
52	8	40.0	10	1	US-10-084-826-44
53	8	40.0	10	1	US-10-223-765-229
54	8	40.0	10	1	US-10-412-105-36
55	8	40.0	10	1	US-10-412-105-36
56	7.4	37.0	9	1	US-10-402-016-2

ALIGNMENTS

RESULT 1
US-09-864-636A-1062
; Sequence 1062, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwail, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1062
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: The residue at this position is linked to a spacer bearing a Cy3
; OTHER INFORMATION: dye
US-09-864-636A-1062

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.8%; Pred. No. 5.1;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 CAACTCTTCGGG 14
||| ||| ||| |||
Db 1 CAACGCTTCGTGG 13

RESULT 2
US-09-864-636A-1187
; Sequence 1187, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwail, Hatim
; APPLICANT: Bartholomay, Christian

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:14:02 ; Search time 0.001 Seconds
(without alignments)
8.960 Million cell updates/sec

Title: US-09-436-060A-7
Perfect score: 20
Sequence: 1 ccaactcttcggtgagcag 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 22 seqs, 224 residues

Total number of hits satisfying chosen parameters: 44

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 22 summaries

Database : rni7.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1	US-08-770-565-7
C 2	10	50.0	11	1	US-07-778-233B-3
C 3	10	50.0	11	1	US-07-963-321-3
C 4	10	50.0	11	1	US-08-290-641-3
C 5	10	50.0	11	1	US-08-548-540-3
C 6	10	50.0	11	1	PCT-US96-09809-3
C 7	8.4	42.0	10	1	US-08-388-353-191
C 8	8.4	42.0	10	1	US-08-488-551B-191
C 9	8	40.0	10	1	US-08-410-116B-21
C 10	8	40.0	10	1	US-08-667-689A-21
C 11	8	40.0	10	1	US-08-712-011-21
C 12	8	40.0	10	1	US-08-478-239A-21
C 13	8	40.0	10	1	US-09-779-233-36
C 14	7.4	37.0	9	1	US-08-850-347-3
C 15	7.4	37.0	9	1	US-08-990-065-3
C 16	7.4	37.0	9	1	US-09-380-532-10
C 17	7.4	37.0	9	1	PCT-US91-03680-137
C 18	7	35.0	8	1	US-09-398-499-22
C 19	7	35.0	8	1	US-09-398-499-45
C 20	7	35.0	9	1	US-08-798-738-3
C 21	7	35.0	9	1	US-10-096-596-33
C 22	6.8	34.0	9	1	PCT-US91-03680-139

ALIGNMENTS

RESULT 1
US-08-770-565-7
; Sequence 7, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo

APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0023000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-7
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.073; 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCAACTCTTCGCGGTGAGCAG 20
Db 1 CCAACTCTTCGCGGTGAGCAG 20
RESULT 2
US-07-778-233B-3/c
; Sequence 3, Application US/07778233B
; Patent No. 5270170
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,233B
FILING DATE: 19911016

10/21/96 @ 10:10

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:37:16 ; Search time 0.001 Seconds
(without alignments)
15.618 Million cell updates/sec

Title: US-09-436-060A-9
Perfect score: 19
Sequence: 1 gctctagaatgaacggtgg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 40 seqs, 411 residues

Total number of hits satisfying chosen parameters: 80

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : rni9.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	1	US-08-770-565-9
2	16.4	86.3	18	1	US-08-974-549A-543
3	16.4	86.3	18	1	US-09-402-181B-543
4	16.4	86.3	18	1	US-09-721-456-543
5	15	78.9	15	1	US-08-770-565-10
6	11	57.9	11	1	US-08-770-565-11
7	10.2	53.7	13	1	PCT-US94-04361-1
8	10	52.6	10	1	US-09-508-753B-391
9	9.4	49.5	12	1	US-08-390-858B-22
10	8.4	44.2	11	1	US-08-390-858B-3
11	8	42.1	9	1	US-08-642-045B-2
12	8	42.1	9	1	US-09-071-353-4
13	8	42.1	9	1	US-08-852-288-4
14	8	42.1	9	1	US-09-428-326-4
15	8	42.1	10	1	US-08-301-872A-28
16	8	42.1	10	1	US-08-301-872A-28
17	8	42.1	10	1	US-08-244-491A-16
18	8	42.1	10	1	US-08-244-491A-16
19	8	42.1	10	1	US-08-161-281A-9
20	8	42.1	10	1	US-08-161-281A-9
21	8	42.1	10	1	US-08-139-882-16
22	8	42.1	10	1	US-08-139-882-16
23	8	42.1	10	1	US-08-797-727A-24
24	8	42.1	10	1	US-08-797-727A-24
25	8	42.1	10	1	US-08-797-727A-25
26	8	42.1	10	1	US-08-797-727A-25
27	8	42.1	10	1	US-08-443-372A-28
28	8	42.1	10	1	US-08-443-372A-28
29	8	42.1	10	1	US-08-189-256A-39
30	8	42.1	10	1	US-08-189-256A-39
31	8	42.1	10	1	US-09-171-878-26
32	8	42.1	10	1	US-09-193-853-39
33	8	42.1	10	1	US-09-193-853-39

34	8	42.1	10	1	US-09-445-283C-64
35	7	36.8	8	1	US-08-244-491A-14
36	7	36.8	8	1	US-08-244-491A-14
37	7	36.8	8	1	US-08-797-727A-22
38	7	36.8	8	1	US-08-797-727A-22
39	7	36.8	8	1	US-08-650-262-21
40	7	36.8	8	1	US-08-650-262-21
41	7	36.8	8	1	US-09-171-878-8
42	7	36.8	8	1	US-09-171-878-8
43	7	36.8	8	1	US-07-845-937A-5
44	7	36.8	8	1	US-07-845-937A-5
45	7	36.8	8	1	US-09-514-245-43
46	6.4	33.7	8	1	US-08-849-075-8
47	6.4	33.7	8	1	US-09-286-098-32
48	6.4	33.7	8	1	US-08-960-774-99
49	6.4	33.7	8	1	US-09-325-193A-26
50	6.4	33.7	8	1	US-09-191-170-32
51	6.4	33.7	8	1	US-09-684-938-97
52	6.4	33.7	8	1	US-09-308-825A-97
53	6.4	33.7	8	1	US-09-337-619-95
54	6.4	33.7	8	1	US-09-940-244-114
55	6	31.6	8	1	US-09-514-245-43

ALIGNMENTS

RESULT 1
US-08-770-565-9
; Sequence 9, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Puzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0023000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 19; DB 1; Length 19;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:35:32 ; Search time 0.001 Seconds

(without alignments)

48.564 Million cell updates/sec

Title: US-09-436-060A-9

Perfect score: 19

Sequence: 1 gcttagaatgaacggtgg 19

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 95 seqs, 1278 residues

Total number of hits satisfying chosen parameters: 190

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 101 summaries

Database: rng9.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	RNA component of h
2	19	100.0	21	1	ADP33824
3	19	100.0	21	1	ADP33812
4	19	100.0	21	1	ADP33832
5	19	100.0	21	1	ADP33816
6	19	100.0	21	1	ADG30043
7	19	100.0	23	1	ADP33794
8	19	100.0	23	1	ADP33793
9	19	100.0	23	1	ADP33828
10	19	100.0	23	1	ADP33820
11	19	100.0	23	1	ADG30039
12	19	100.0	23	1	ADG39525
13	19	100.0	23	1	ADG39524
14	19	100.0	25	1	AZ828704
15	17	89.5	21	1	ADP33831
16	17	89.5	21	1	ADP33811
17	17	89.5	21	1	ADP33823
18	17	89.5	21	1	ADG30042
19	17	89.5	21	1	AAV41177
20	15	78.9	15	1	AAS15931
21	14	73.7	15	1	AAS15930
22	13	68.4	13	1	AAV41178
23	11	57.9	11	1	AAS15929
24	11	57.9	11	1	ABH78027
25	10.4	54.7	12	1	ABH78027
26	10.4	54.7	12	1	ABH78027
27	10.4	54.7	12	1	ABH78027
28	10.4	54.7	12	1	ABH78027
29	10.4	54.7	13	1	ABF48447
30	10.4	54.7	13	1	ABF48447
31	10.4	54.7	13	1	ABF48447
32	10.4	54.7	13	1	ABF48447
33	10.4	54.7	13	1	ABH46944

ALIGNMENTS

C 34	10.4	54.7	13	1	ABH46945
C 35	10.4	54.7	13	1	ABF98323
C 36	10.4	54.7	13	1	ABC95736
C 37	10.4	54.7	13	1	ABF87423
C 38	10.2	53.7	13	1	AAQ72951
C 39	10.2	53.7	13	1	ABF72559
C 40	10	52.6	12	1	ABK72570
C 41	10	52.6	12	1	ABF40449
C 42	10	52.6	13	1	ABF40448
C 43	9.8	51.6	13	1	ABF72558
C 44	9.8	51.6	13	1	ABF72559
C 45	9.8	51.6	13	1	ADOS8258
C 46	9.4	49.5	11	1	ABV67536
C 47	9.4	49.5	11	1	ABV64776
C 48	9.4	49.5	11	1	ADQ33761
C 49	9.4	49.5	11	1	ADQ34226
C 50	9.4	49.5	12	1	ABI14095
C 51	9.4	49.5	12	1	ABI175975
C 52	9.4	49.5	12	1	ABI121545
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C 54	9	47.4	10	1	AAF34756
C 55	9	47.4	11	1	ABV71216
C 56	9	47.4	11	1	ABV63795
C 57	9	47.4	12	1	ABI177502
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C 59	9	47.4	12	1	ABI134553
C 60	9	47.4	12	1	ABH82778
C 61	9	47.4	12	1	ABI157594
C 62	8.4	44.2	10	1	AAZ93934
C 63	8.4	44.2	10	1	AAZ78267
C 64	8.4	44.2	10	1	AAZ83713
C 65	8.4	44.2	10	1	ABQ75142
C 66	8.4	44.2	10	1	ADB88808
C 67	8.4	44.2	11	1	AAT79837
C 68	8.4	44.2	11	1	ABQ87675
C 69	8.4	44.2	11	1	ABV87726
C 70	8.4	44.2	11	1	ABV86612
C 71	8.4	44.2	11	1	ADQ80074
C 72	8.4	44.2	11	1	ADQ35743
C 73	8.4	44.2	11	1	ADQ35622
C 74	8.4	44.2	11	1	ADQ32520
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C 77	8	42.1	10	1	AAV35994
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C 87	8	42.1	10	1	AAH20937
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C 93	8	42.1	10	1	AAH20937
C 94	8	42.1	10	1	AAH20937
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C 97	8	42.1	10	1	AAH20937
C 98	8	42.1	10	1	AAH20937
C 99	8	42.1	10	1	AAH20937
C 100	8	42.1	10	1	AAH20937
C 101	8	42.1	10	1	AAH20937

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:33:54 ; Search time 0.001 Seconds
(without alignments)
23.636 Million cell updates/sec

Title: US-09-436-060A-9

Perfect score: 19
Sequence: 1 gctctagaatgaacggtgg 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 54 seqs, 622 residues

Total number of hits satisfying chosen parameters: 108

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : rge9.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
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3	19	100.0	25	1	BD023705
4	16.4	86.3	18	1	BD131326
5	16.4	86.3	18	1	E36993
6	16.4	86.3	18	1	AR390670
7	16.4	86.3	18	1	AR330284
8	16.4	86.3	18	1	AX810578
9	15	78.9	15	1	BD011244
10	15	78.9	15	1	AR063834
11	11	57.9	11	1	BD023706
12	11	57.9	11	1	AR063835
13	10.4	54.7	12	1	AX456436
14	10	52.6	10	1	AR303666
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16	9.4	49.5	11	1	CO837258
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28	8.4	44.2	11	1	AX471853
29	8.4	44.2	11	1	AX627357
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32	8	42.1	9	1	BD106461
33	8	42.1	10	1	AR25264

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C 35	8	42.1	10	1	AR027091
C 36	8	42.1	10	1	AR027091
C 37	8	42.1	10	1	AR027092
C 38	8	42.1	10	1	AR027092
C 39	8	42.1	10	1	AR023385
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C 45	8	42.1	10	1	I45921
C 46	8	42.1	10	1	I45921
C 47	8	42.1	10	1	I89756
C 48	8	42.1	10	1	I89756
C 49	8	42.1	10	1	AR403889
C 50	8	42.1	10	1	AX205086
C 51	8	42.1	10	1	AX205086
C 52	8	42.1	10	1	AX259320
C 53	8	42.1	10	1	AX259320
C 54	7.4	38.9	9	1	AX205239
C 55	7	36.8	7	1	BD023708
C 56	7	36.8	8	1	E17002
C 57	7	36.8	8	1	E17002
C 58	7	36.8	8	1	E17034
C 59	7	36.8	8	1	E17034
C 60	7	36.8	8	1	E17045
C 61	7	36.8	8	1	E17045
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C 63	7	36.8	8	1	E41637
C 64	7	36.8	8	1	AX003296
C 65	7	36.8	8	1	BD092167
C 66	7	36.8	8	1	BD092167
C 67	7	36.8	9	1	A70966
C 68	7	36.8	9	1	S98713
C 69	6.4	33.7	9	1	A70966
C 70	6	31.6	8	1	AX003296

ALIGNMENTS

AR063833 Sequence 9 from patent US 5846723. 19 bp DNA linear PAT 29-SEP-1999

LOCUS AR063833.1 GI:5993141

DEFINITION

AR063833

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

100.0%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACCGTGG 19

DB 1 GCTCTAGATGACCGTGG 19

RESULT 2

BD023705

LOCUS

BD023705

19 bp DNA linear PAT 27-AUG-2002

Kim, N.Woo., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.
Methods for detecting the RNA component of telomerase
Patent: US 5846723-A 9 08-DEC-1998;

Location/Qualifiers

1..19

/organism="unknown"

/mol_type="unassigned DNA"

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:29:42 ; Search time 0.001 Seconds
(without alignments)
8.880 Million cell updates/sec

Title: US-09-436-060A-10
Perfect score: 15
Sequence: 1 gctctagaatgaacg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 34 seqs, 296 residues

Total number of hits satisfying chosen parameters: 68

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 39 summaries

Database : rnpb10.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	8.4	56.0	10	1	US-10-033-145-695
C 2	8.4	56.0	11	1	US-10-450-797-1430
C 3	8	53.3	8	1	US-10-027-632-52787
C 4	8	53.3	8	1	US-10-027-632-52787
C 5	8	53.3	9	1	US-10-027-632-70835
C 6	8	53.3	9	1	US-10-027-632-70835
C 7	8	53.3	9	1	US-10-345-859-4
C 8	8	53.3	10	1	US-10-663-241-64
C 9	7.6	50.7	10	1	US-10-027-632-81746
C 10	7.6	50.7	10	1	US-10-027-632-81746
C 11	7.4	49.3	9	1	US-10-310-294-22
C 12	7.4	49.3	9	1	US-10-182-327-131
C 13	7.4	49.3	9	1	US-10-669-841-11237
C 14	7.4	49.3	9	1	US-10-673-938-154
C 15	7	46.7	7	1	US-10-310-294-16
C 16	7	46.7	7	1	US-10-310-294-16
C 17	7	46.7	7	1	US-10-669-841-11231
C 18	7	46.7	8	1	US-10-160-232-57
C 19	7	46.7	8	1	US-10-160-232-57
C 20	7	46.7	8	1	US-10-310-294-17
C 21	7	46.7	8	1	US-10-310-294-20
C 22	7	46.7	8	1	US-10-425-668-9
C 23	7	46.7	8	1	US-10-425-668-9
C 24	7	46.7	8	1	US-10-682-420-43
C 25	7	46.7	8	1	US-10-409-613-43
C 26	7	46.7	8	1	US-10-442-180-43
C 27	7	46.7	8	1	US-10-669-841-11232
C 28	7	46.7	8	1	US-10-669-841-11235
C 29	7	46.7	8	1	US-10-757-345-60
C 30	7	46.7	9	1	US-10-310-294-21
C 31	7	46.7	9	1	US-10-310-294-24
C 32	7	46.7	9	1	US-10-310-294-83
C 33	7	46.7	9	1	US-10-310-294-107
C 34	7	46.7	9	1	US-10-669-841-11236

C 34 7 46.7 9 1 US-10-669-841-11239 Sequence 11239, A
C 35 7 46.7 9 1 US-10-669-841-11238 Sequence 11238, A
C 36 7 46.7 9 1 US-10-669-841-11321 Sequence 11321, A
C 37 6 40.0 8 1 US-10-682-420-43 Sequence 43, Appl
C 38 6 40.0 8 1 US-10-409-613-43 Sequence 43, Appl
C 39 6 40.0 8 1 US-10-442-180-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-10-033-145-695/c
; Sequence 695, Application US/10033145
; Publication No. US2002015151SA1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 695
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-695

Query Match 56.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCTAGAATG 11
DB 10 CTCTGAATG 1

RESULT 2

US-10-450-797-1430/c
; Sequence 1430, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1430
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1430

Query Match 56.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGAATGAACG 15
DB 10 AGAATGAACG 1

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:28:22 : Search time 0.001 Seconds
(without alignments)
8.970 Million cell updates/sec

Title: US-09-436-060A-10
Perfect score: 15
Sequence: 1 gctctagaatgaacg 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 30 seqs, 299 residues

Total number of hits satisfying chosen parameters: 60

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : rni10.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	100.0	15	1	US-08-770-565-10
2	15	100.0	19	1	US-08-770-565-9
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4	10.2	68.0	13	1	PCR-US94-04361-1
5	9.4	62.7	12	1	US-08-390-858B-22
6	8.4	56.0	11	1	US-08-390-858B-3
7	8	53.3	9	1	US-09-071-353-4
8	8	53.3	9	1	US-09-426-325-4
9	8	53.3	10	1	US-08-301-872A-28
10	8	53.3	10	1	US-08-301-872A-28
11	8	53.3	10	1	US-08-244-491A-16
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22	8	53.3	10	1	US-08-443-372A-28
23	8	53.3	10	1	US-08-189-256A-39
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26	8	53.3	10	1	US-09-193-853-39
27	8	53.3	10	1	US-09-193-853-39
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31	7	46.7	8	1	US-08-397-727A-22
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c	35	7	46.7	8	1	US-09-171-878-8	Sequence 8, Appl
c	36	7	46.7	8	1	US-09-171-878-8	Sequence 8, Appl
c	37	7	46.7	8	1	US-07-845-937A-5	Sequence 5, Appl
c	38	7	46.7	8	1	US-07-845-937A-5	Sequence 5, Appl
c	39	7	46.7	8	1	US-09-514-245-43	Sequence 43, Appl
c	40	7	46.7	9	1	US-08-642-045B-2	Sequence 2, Appl
c	41	7	46.7	9	1	US-08-852-268-4	Sequence 4, Appl
c	42	6.4	42.7	8	1	US-09-684-938-97	Sequence 97, Appl
c	43	6.4	42.7	8	1	US-09-308-825A-97	Sequence 97, Appl
c	44	6.4	42.7	8	1	US-09-340-244-114	Sequence 114, Appl
c	45	6	40.0	8	1	US-09-514-245-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-10
; Sequence 10, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Fruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-10

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 1 GCTCTAGATGAACG 15
Db 1 GCTCTAGATGAACG 15

RESULT 2
US-08-770-565-9

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:27:00 ; Search time 0.001 Seconds

(without alignments)
17.490 Million cell updates/sec

Title: US-09-436-060A-10

Perfect score: 15

Sequence: 1 gctctagaatgaacg 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 53 seqs, 583 residues

Total number of hits satisfying chosen parameters: 106

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 59 summaries

Database : rng10.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	1 AAV41177	RNA component of h
2	15	100.0	19	1 AAV41176	RNA component of h
3	13	86.7	13	1 AAS15930	Human telomerase p
4	11	73.3	11	1 AAV41178	RNA component of h
5	11	73.3	11	1 AAS15929	Human telomerase p
6	10.4	69.3	12	1 ABL39311	Synthetic luciferase
7	10.2	68.0	13	1 AAV72951	Erythropoietin con
8	10	66.7	12	1 ABL27364	Oligonucleotide pr
9	10	66.7	12	1 ABL72570	Human OPAL Gene, e
10	9.8	65.3	13	1 ADO58258	Hepatitis A Genome
11	9.4	62.7	11	1 ABV67536	Human skin EST 532
12	9.4	62.7	11	1 ADQ34226	Human facial skin-
13	9.4	62.7	12	1 ABL78027	Oligonucleotide pr
14	9	60.0	10	1 AAD05873	Human cholinergic
15	9	60.0	10	1 AAF34756	Yeast NORF gene SA
16	9	60.0	11	1 ABV71216	Human skin EST 900
17	9	60.0	11	1 ABV63795	Human skin EST 158
18	9	60.0	12	1 ABL77502	Oligonucleotide pr
19	9	60.0	12	1 ABL50973	Oligonucleotide pr
20	9	60.0	12	1 ABL34553	Oligonucleotide pr
21	9	60.0	12	1 ABL67594	Oligonucleotide pr
22	9	60.0	12	1 ABL78267	Human dendritic ce
23	8.4	56.0	10	1 AAZ83713	Metastatic breast
24	8.4	56.0	10	1 AAT79837	Bcl-2 inhibitory e
25	8.4	56.0	11	1 ABL79837	Human skin stress/
26	8.4	56.0	11	1 ABL79837	Human skin EST 256
27	8.4	56.0	11	1 ABL79837	Human skin EST 551
28	8.4	56.0	11	1 ABL79837	Human skin EST 439
29	8.4	56.0	11	1 ABL79837	Human alpha la adr
30	8.4	56.0	11	1 ABL79837	Human facial skin-
31	8.4	56.0	11	1 ABL79837	Human facial skin-
32	8.4	56.0	11	1 ABL79837	Xba I linker. Syn
33	8	53.3	10	1 AAV41177	RNA component of human telomerase (hTR) antisense oligo 21ab3.

C 34	8	53.3	10	1	AAQ98160	Xba I linker. Syn
C 35	8	53.3	10	1	AAV35994	Primer used in RAP
C 36	8	53.3	10	1	AAZ8584	Metastatic breast
C 37	8	53.3	10	1	AAZ86135	Metastatic breast
C 38	8	53.3	10	1	AAH48687	Rabbit GNTI linker
C 39	8	53.3	10	1	AAH48687	Rabbit GNTI linker
C 40	8	53.3	10	1	AAH48687	Endoplasmic reticu
C 41	8	53.3	10	1	AAH48687	Endoplasmic reticu
C 42	8	53.3	10	1	AAH48687	scFv(ox) antibody
C 43	8	53.3	10	1	AAH48687	scFv(ox) antibody
C 44	8	53.3	10	1	AAH20937	Anaerobically-indu
C 45	8	53.3	10	1	AAH20937	Anaerobically-indu
C 46	8	53.3	10	1	AAH20937	Yeast NORF gene SA
C 47	8	53.3	10	1	AAH20937	Yeast NORF gene SA
C 48	8	53.3	10	1	AAH20937	Yeast NORF gene SA
C 49	8	53.3	10	1	AAH20937	Yeast NORF gene SA
C 50	8	53.3	10	1	AAH20937	Yeast NORF gene SA
C 51	8	53.3	10	1	AAH20937	Yeast NORF gene SA
C 52	8	53.3	10	1	AAH20937	Yeast NORF gene SA
C 53	8	53.3	10	1	AAH20937	Yeast NORF gene SA
C 54	8	53.3	10	1	AAH20937	Plasmid pRT100/scF
C 55	8	53.3	10	1	AAH20937	Plasmid pRT100/scF
C 56	8	53.3	10	1	AAH20937	Human UBE3A gene A
C 57	8	53.3	10	1	AAH20937	Human CYP2D6 gene
C 58	7.4	49.3	9	1	AAH20937	Human glioma endot
C 59	7.4	49.3	9	1	AAH20937	Sequence capable o
C 60	7.4	49.3	9	1	AAH20937	HBV RT primer deco

ALIGNMENTS

RESULT 1

AAV41177

ID AAV41177 standard; DNA; 15 BP.

XX AC AAV41177;

XX XX

DT 08-OCT-1998 (first entry)

XX XX

DE RNA component of human telomerase (hTR) antisense oligo 21ab3.

XX RNA component; human telomerase; antisense oligonucleotide; infection;
neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
contraception; sterilization; immunosuppression; therapeutic; hTR;
immune system down-regulation; anti-inflammatory therapy; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9828442-A1.

XX PD 02-JUL-1998.

XX PF 19-DEC-1997; 97WO-US023619.

XX PR 20-DEC-1996; 96US-00770564.

XX PR 20-DEC-1996; 96US-00770565.

XX PA (GERO-) GERON CORP.

XX PI Kim NW, Wu F, Kealey JT, Pruzan R, Weinrich SL;

XX WPI; 1998-377670/32.

XX DR New polynucleotide(s) antisense to human telomerase - used for detecting

XX PT or inhibiting human telomerase, e.g. for treating cancers, contraception,

XX PS immuno-suppression or treating infection.

XX CC Claim 11; Page 65; 80pp; English.

XX CC Sequences shown in AAV41189 to AAV41181 represent antisense

XX CC oligonucleotides to the RNA component of human telomerase (hTR). These

XX CC antisense oligonucleotides specifically hybridize to a nucleotide

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:19:42, Search time 0.001 Seconds
(without alignments)
13.650 Million cell updates/sec

Title: US-09-436-060A-10

Perfect score: 15

Sequence: 1 gctctagaatgaacg 15

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 0.5

Searched: 43 seqs, 455 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 59 summaries

Database: rge10.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	1	AR063834
2	15	100.0	15	1	BD023706
3	15	100.0	19	1	AR063833
4	15	100.0	19	1	BD023705
5	11	73.3	11	1	AR063835
6	11	73.3	11	1	BD023707
7	10.4	69.3	12	1	AX456436
8	9.4	62.7	11	1	CQ837258
9	9.4	62.7	11	1	AX628281
10	9.4	62.7	12	1	I50791
11	9	60.0	11	1	AX624540
12	9	60.0	11	1	AX631961
13	8.4	56.0	10	1	BD239277
14	8.4	56.0	11	1	AX635552
15	8.4	56.0	11	1	CQ836793
16	8.4	56.0	11	1	I50773
17	8.4	56.0	11	1	AX471853
18	8.4	56.0	11	1	AX625521
19	8.4	56.0	11	1	AX627357
20	8.4	56.0	11	1	AX628471
21	8	53.3	9	1	A83648
22	8	53.3	9	1	BD106461
23	8	53.3	10	1	A25264
24	8	53.3	10	1	A25264
25	8	53.3	10	1	AR027091
26	8	53.3	10	1	AR027091
27	8	53.3	10	1	AR027092
28	8	53.3	10	1	AR027092
29	8	53.3	10	1	AR032385
30	8	53.3	10	1	AR032385
31	8	53.3	10	1	AR160668
32	8	53.3	10	1	I40153
33	8	53.3	10	1	I40153

34	8	53.3	10	1	I45921
35	8	53.3	10	1	I45921
36	8	53.3	10	1	I89756
37	8	53.3	10	1	I89756
38	8	53.3	10	1	AR403689
39	8	53.3	10	1	AX205086
40	8	53.3	10	1	AX205086
41	8	53.3	10	1	AX259320
42	8	53.3	10	1	AX259320
43	7.4	49.3	9	1	AX205239
44	7	46.7	7	1	BD023708
45	7	46.7	8	1	E17002
46	7	46.7	8	1	E17002
47	7	46.7	8	1	E17034
48	7	46.7	8	1	E17034
49	7	46.7	8	1	E17045
50	7	46.7	8	1	E17045
51	7	46.7	8	1	E41637
52	7	46.7	8	1	E41637
53	7	46.7	8	1	AX003296
54	7	46.7	8	1	BD092167
55	7	46.7	8	1	BD092167
56	7	46.7	9	1	A70966
57	7	46.7	9	1	S98713
58	6.4	42.7	9	1	A70966
59	6	40.0	8	1	AX003296

ALIGNMENTS

RESULT 1
AR063834
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AR063834
Sequence 10 from patent US 5846723.
AR063834
AR063834.1 GI:5993142
Unknown.
Unknown.
Unclassified.
Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
Methods for detecting the RNA component of telomerase
Patent: US 5846723-A 10 08-DEC-1998;
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

linear PAT 29-SEP-1999

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGACG 15
| | | | | | | | | | | | | | |
Db 1 GCTCTAGATGACG 15

RESULT 2
BD023706
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

BD023706
Method for detecting and inhibiting RNA component of telomerase.
BD023706
BD023706.1 GI:22564929
JP 2001507229-A/10.
unidentified
unidentified
unclassified.
1 (bases 1 to 15)
Kim,N.W., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
Method for detecting and inhibiting RNA component of telomerase
Patent: JP 2001507229-A 10 05-JUN-2001;

linear PAT 27-AUG-2002

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:12:40 ; Search time 0.001 Seconds
(without alignments)
5.720 Million cell updates/sec

Title: US-09-436-060A-11
Perfect score: 11
Sequence: 1 GCTCTAGATG 11

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 29 seqs, 260 residues

Total number of hits satisfying chosen parameters: 58

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 47 summaries

Database: rni11.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	1	US-08-770-565-11
2	9.4	85.5	12	1	US-08-390-858B-22
3	8	72.7	9	1	US-09-071-353-4
4	8	72.7	9	1	US-09-426-326-4
5	8	72.7	10	1	US-08-301-872A-28
6	8	72.7	10	1	US-08-301-872A-28
7	8	72.7	10	1	US-08-244-491A-16
8	8	72.7	10	1	US-08-244-491A-16
9	8	72.7	10	1	US-08-161-281A-9
10	8	72.7	10	1	US-08-139-862-16
11	8	72.7	10	1	US-08-139-862-16
12	8	72.7	10	1	US-08-797-727A-24
13	8	72.7	10	1	US-08-797-727A-24
14	8	72.7	10	1	US-08-797-727A-25
15	8	72.7	10	1	US-08-797-727A-25
16	8	72.7	10	1	US-08-443-372A-28
17	8	72.7	10	1	US-08-443-372A-28
18	8	72.7	10	1	US-08-189-356A-39
19	8	72.7	10	1	US-08-189-356A-39
20	8	72.7	10	1	US-08-171-878-8
21	8	72.7	10	1	US-08-171-878-8
22	8	72.7	10	1	US-09-193-853-39
23	8	72.7	10	1	US-09-193-853-39
24	7	63.6	8	1	US-08-244-491A-14
25	7	63.6	8	1	US-08-244-491A-14
26	7	63.6	8	1	US-08-797-727A-22
27	7	63.6	8	1	US-08-797-727A-22
28	7	63.6	8	1	US-08-650-262-21
29	7	63.6	8	1	US-08-650-262-21
30	7	63.6	8	1	US-09-171-878-8
31	7	63.6	8	1	US-09-171-878-8
32	7	63.6	8	1	US-07-845-937A-5
33	7	63.6	8	1	US-07-845-937A-5

34 7 63.6 8 1 US-09-514-245-43 Sequence 43, Appl
C 35 6.4 58.2 8 1 US-08-684-938-97 Sequence 97, Appl
C 36 6.4 58.2 8 1 US-09-308-825A-97 Sequence 97, Appl
C 37 6.4 58.2 8 1 US-09-940-244-114 Sequence 114, Appl
38 6 54.5 7 1 US-09-117-122-2 Sequence 2, Appl
C 39 6 54.5 7 1 US-09-117-122-2 Sequence 2, Appl
C 40 6 54.5 8 1 US-09-514-245-43 Sequence 43, Appl
C 41 6 54.5 8 1 US-09-041-675-1 Sequence 1, Appl
C 42 6 54.5 8 1 US-09-041-675-1 Sequence 1, Appl
C 43 6 54.5 8 1 US-09-041-675-16 Sequence 16, Appl
C 44 6 54.5 8 1 US-09-041-675-16 Sequence 16, Appl
C 45 6 54.5 8 1 US-08-290-736C-13 Sequence 13, Appl
C 46 6 54.5 8 1 US-09-054-832-11 Sequence 11, Appl
C 47 6 54.5 8 1 US-09-640-953-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-11
; Sequence 11, Application US/08770565
; Patent No 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weirich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0023000US
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-11

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.38;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11

Db 1 GCTCTAGATG 11

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:11:07 ; Search time 0.001 Seconds
(without alignments)
6.446 Million cell updates/sec

Title: US-09-436-060A-11
Perfect score: 11
Sequence: 1 gctctagaatg 11

Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 0.5

Searched: 30 seqs, 293 residues

Total number of hits satisfying chosen parameters: 60

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 42 summaries

Database : rng11.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	1 AAV41178	RNA component of h
2	11	100.0	11	1 AAG15929	Human telomerase p
3	11	100.0	13	1 AAG15930	Human telomerase p
4	10	90.9	12	1 ABL99311	Synthetic lucifera
5	9	81.8	10	1 AAF34756	Yeast NORF gene SA
6	8.4	76.4	10	1 AAZ78267	Human dendritic ce
7	8.4	76.4	11	1 ABV66612	Human skin ESR 439
8	8.4	76.4	11	1 ADQ32520	Human facial skin-
9	8	72.7	10	1 AAQ98160	Xba I linker. Syn
10	8	72.7	10	1 AAQ98160	Xba I linker. Syn
11	8	72.7	10	1 AAV35994	Primer used in RAP
12	8	72.7	10	1 AA236584	Metastatic breast
13	8	72.7	10	1 AA236135	Metastatic breast
14	8	72.7	10	1 AAH48687	Rabbit Gnt1 linker
15	8	72.7	10	1 AAH48687	Rabbit Gnt1 linker
16	8	72.7	10	1 AAH49493	Endoplasmic reticu
17	8	72.7	10	1 AAH49493	Endoplasmic reticu
18	8	72.7	10	1 AAH49475	scFv(ox) antibody
19	8	72.7	10	1 AAH49475	scFv(ox) antibody
20	8	72.7	10	1 AAH20937	Anaerobically-indu
21	8	72.7	10	1 AAH20937	Anaerobically-indu
22	8	72.7	10	1 AAF41400	Yeast NORF gene SA
23	8	72.7	10	1 AAF41399	Yeast NORF gene SA
24	8	72.7	10	1 AAF36297	Yeast NORF gene SA
25	8	72.7	10	1 AAF41401	Yeast NORF gene SA
26	8	72.7	10	1 AA169335	Plasmid pRT100/scF
27	8	72.7	10	1 AA169335	Plasmid pRT100/scF
28	8	72.7	10	1 AAQ72361	Human CYP2D6 gene
29	7	63.6	7	1 AAV41179	RNA component of h
30	7	63.6	8	1 AAZ87757	Anti-human VEGF re
31	7	63.6	8	1 AAZ87757	Anti-human VEGF re
32	7	63.6	8	1 AAF70230	Flt-1 related DNA
33	7	63.6	8	1 AAF70230	Flt-1 related DNA

34 7 63.6 8 1 ABK29963 Hepatitis B virus
35 7 63.6 8 1 ABK29963 Hepatitis B virus
36 7 63.6 9 1 AAV28804 Primer extension p
37 7 63.6 10 1 AAF34756 Yeast NORF gene SA
38 6.4 58.2 8 1 AAF76716 Miniprobe oligonuc
39 6.4 58.2 8 1 AAV65875 Miniprobe oligonuc
40 6.4 58.2 8 1 ABK29965 Hepatitis B virus
41 6.4 58.2 9 1 AAV28804 Primer extension p
42 6 54.5 8 1 ABK29965 Hepatitis B virus

ALIGNMENTS

RESULT 1
AAV41178
ID AAV41178 standard; DNA; 11 BP.
XX
AC AAV41178;
XX
DT 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 21ab2.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN W09828442-AL.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US023619.
XX
PR 20-DEC-1996; 96US-00770564.
PR 20-DEC-1996; 96US-00770565.
XX
(GERO-) GERON CORP.
XX
Klm NW, Wu F, Kealey JT, Pruzan R, Weinrich SL;
XX
WPI; 1998-377670/32.
XX
New polynucleotide(s) anti-sense to human telomerase - used for detecting
or inhibiting human telomerase, e.g. for treating cancers, contraception,
immuno-suppression or treating infection.

Claim 11; Page 65; 80pp; English.

Sequences shown in AAV41169 to AAV41181 represent antisense oligonucleotides to the RNA component of human telomerase (hTR). These antisense oligonucleotides specifically hybridise to a nucleotide sequence within an accessible region of the hTR, but that does not hybridise to a sequence within the template region of hTR. These oligonucleotides may specifically be used for detection of an RNA component of human telomerase in a sample. This is useful for diagnosing cancer (especially neuroblastoma, bladder, colon and prostate cancer), and providing prognosis for a cancer patient. The inhibitory oligonucleotides can inhibit the telomerase activity level in a cell by interfering with transcription of the RNA component, decreasing the half-life of the telomerase RNA component transcript, inhibiting assembly of the RNA component into the telomerase holoenzyme, or inhibiting the polymerase activity of telomerase. These antisense oligonucleotides can be used for inhibiting telomerase activity in both cultured cells and in cells in vivo. They can be used in therapeutics for treating or preventing cancer, for contraception or sterilisation, for immunosuppression, and for selectively down-regulating specific branches of the immune system, e.g. a specific subset of T-cells, in anti-inflammatory therapies or for treating infections by, e.g. yeast.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:08:37 ; Search time 0.001 Seconds
(without alignments)
7.150 Million cell updates/sec

Title: US-09-436-060A-11

Perfect score: 11
Sequence: 1 gctctagaatg 11

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 35 seqs, 325 residues

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 53 summaries

Database : rgell.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	AR063835	ACCESSION:AR063835
2	11	100.0	11	BD023707	ACCESSION:BD023707
3	10	90.9	12	AX456436	ACCESSION:AX456436
4	9.4	85.5	12	I50791	ACCESSION:I50791
5	8.4	76.4	10	BD239277	ACCESSION:BD239277
6	8.4	76.4	11	CQ835552	ACCESSION:CQ835552
7	8.4	76.4	11	AX627357	ACCESSION:AX627357
8	8	72.7	9	A83648	ACCESSION:A83648
9	8	72.7	9	BD106461	ACCESSION:BD106461
10	8	72.7	10	A25264	ACCESSION:A25264
11	8	72.7	10	A25264	ACCESSION:A25264
12	8	72.7	10	AR027091	ACCESSION:AR027091
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14	8	72.7	10	AR027092	ACCESSION:AR027092
15	8	72.7	10	AR027092	ACCESSION:AR027092
16	8	72.7	10	AR02385	ACCESSION:AR02385
17	8	72.7	10	AR02385	ACCESSION:AR02385
18	8	72.7	10	AR160668	ACCESSION:AR160668
19	8	72.7	10	I40153	ACCESSION:I40153
20	8	72.7	10	I40153	ACCESSION:I40153
21	8	72.7	10	I45921	ACCESSION:I45921
22	8	72.7	10	I45921	ACCESSION:I45921
23	8	72.7	10	I89756	ACCESSION:I89756
24	8	72.7	10	I89756	ACCESSION:I89756
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27	8	72.7	10	AX259320	ACCESSION:AX259320
28	8	72.7	10	AX259320	ACCESSION:AX259320
29	7	63.6	7	BD023708	ACCESSION:BD023708
30	7	63.6	8	E17002	ACCESSION:E17002
31	7	63.6	8	E17002	ACCESSION:E17002
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36      7 63.6      8 1 E1637       ACCESSION:E1637
C 37      7 63.6      8 1 E1637       ACCESSION:E1637
38      7 63.6      8 1 AX003296     ACCESSION:AX003296
39      7 63.6      8 1 BD092167     ACCESSION:BD092167
C 40      7 63.6      8 1 BD092167     ACCESSION:BD092167
C 41      7 63.6      9 1 A70966      ACCESSION:A70966
C 42      7 63.6      9 1 S98713      ACCESSION:S98713
C 43      6.4 58.2      8 1 AX059000     ACCESSION:AX059000
44      6.4 58.2      8 1 AX059001     ACCESSION:AX059001
45      6.4 58.2      9 1 A70966      ACCESSION:A70966
46      6.2 56.4      8 1 AX059000     ACCESSION:AX059000
C 47      6 54.5      8 1 AX003296     ACCESSION:AX003296
C 48      6 54.5      8 1 AX059001     ACCESSION:AX059001
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ALIGNMENTS

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RESULT 1
AR063835
LOCUS      AR063835      11 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5846723.
ACCESSION AR063835
VERSION    AR063835.1 GI:5993143
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE       Methods for detecting the RNA component of telomerase
JOURNAL     Patent: US 5846723-A 11 08-DEC-1998;
FEATURES    Location/Qualifiers
             1..11
             /organism="unknown"
             /mol_type="unassigned DNA"

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Query Match      100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. NO. 1.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCTCTAGAATG 11
        |||
Db      1 GCTCTAGAATG 11

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RESULT 2
BD023707
LOCUS      BD023707      11 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Method for detecting and inhibiting RNA component of telomerase.
ACCESSION BD023707
VERSION    BD023707.1 GI:22564930
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unclassified.

```

```

REFERENCE   1 (bases 1 to 11)
AUTHORS    Kim,N.W., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE       Method for detecting and inhibiting RNA component of telomerase
JOURNAL     Patent: JP 2001507229-A 11 05-JUN-2001;
COMMENT     GERON CORP
            JP 2001507229-A/11
            PD 05-JUN-2001
            PF 19-DEC-1997 JP 1998529003
            PR 20-DEC-1996 US 08/770564,20-DEC-1996 US 08/770565 PI
            NAM WOO KIM,FRED WU,JAMES T KEALEY,RONALD PRUZAN,SCOTT L PI

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